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An integrated genetic map of the African human malaria vector mosquito, *Anopheles gambiae*.

Zheng L, Benedict MQ, Cornel AJ, Collins FH, Kafatos FC.

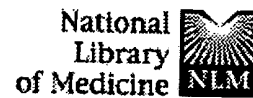
Department of Molecular and Cellular Biology, Harvard University, Cambridge, Massachusetts 02138, USA.

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We present a genetic map based on microsatellite polymorphisms for the African human malaria vector, *Anopheles gambiae*. Polymorphisms in laboratory strains were detected for 89% of the tested microsatellite markers. Genotyping was performed for individual mosquitos from 13 backcross families that included 679 progeny. Three linkage groups were identified, corresponding to the three chromosomes. We added 22 new markers to the existing X chromosome map, for a total of 46 microsatellite markers spanning a distance of 48.9 cM. The second chromosome has 57 and the third 28 microsatellite markers spanning a distance of 72.4 and 93.7 cM, respectively. The overall average distance between markers is 1.6 cM (or 1.1, 1.2, and 3.2 cM for the X, second, and third chromosomes, respectively). In addition to the 131 microsatellite markers, the current map also includes a biochemical selectable markers, Dieltrin resistance (DI), on the second chromosome and five visible markers, pink-eye (p) and white (w) on the X, collarless (c) and lunate (lu) on the second, and red-eye (r) on the third. The cytogenetic locations on the nurse cell polytene chromosomes have been determined for 47 markers, making this map an integrated tool for cytogenetic, genetic, and molecular analysis.

PMID: 8725240 [PubMed - indexed for MEDLINE]

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